

FIG. 1

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LINKER #1 15bp SV40 ORIGIN=332bp  
GACGTCGCGG CCGCTCTAGG CCTCCAAAA AGCCTCCTCA CTACTTCTGG AATAGCTCAG 60  
AGGCCGAGGC GGCCTCGGCC TCTGCATAAA TAAAAAAAT TAGTCAGCCA TGCATGGGGC 120  
GGAGAATGGG CGGAACCTGGG CGGAGTTAGG GCGGGGATGG GCGGAGTTAG GGGCGGGACT 180  
ATGGTTGCTG ACTAATTGAG ATGCATGCTT TGCATACTTC TGCTGCTGG GGAGCCTGGG 240  
GACTTTCCAC ACCTGGTTGC TGAATAATTG AGATGCATGC TTTGCATACT TCTGCCTGCT 300  
GGGGAGCCTG GGGACTTTCC ACACCCTAAC TGACACACAT TCCACAGAA TAATTCCCT 360  
AGTTATTAAT AGTAATCAAT TACGGGGTCA TTAGTTCATA GCCCATATAT GGAGTTCCGC 420  
GTTACATAAC TTACGGTAAA TGGCCCGCCT GGCTGACCGC CCAACGACCC CCGCCCATTTG 480  
CMV PROMOTER-ENHANCER=567bp  
ACGTCAATAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA TTGACGTCAA 540  
TGGGTGGACT ATTTACGGTA AACTGCCAC TTGGCAGTAC ATCAAGTGTA TCATATGCCA 600  
AGTACGCCCC CTATTGACGT CAATGACGGT AAATGGCCCC CTGGCATTAT TGCCACGTAC 660  
ATGACCTTAT GGGACTTTCC TACTTGCCAG TACATCTACG TATTAGTCAT CGCTATTACC 720  
ATGGTGATGC GGTTTTGCCA GTACATCAAT GGGCGTGGAT AGCGGTTTGA CTCACGGGGA 780  
TTTCCAAGTC TCCACCCCAT TGACGTCAAT GGGAGTTTGT TTTGGCACCA AAATCAACGG 840  
GACTTTCCAA AATGTCGTAA CAACTCCGCC CCATTGACGC AAATGGGCGG TAGGCGTGTA 900  
LINKER #3=76bp  
CGGTGGGAGG TCTATATAAG CAGAGCTGGG TACGTGAACC GTCAGATCGC CTGGAGACGC 960  
CATCACAGAT CTCTCACCAT GAGGGTCCCC GCTCAGCTCC TGGGGCTCTT GGCTGCTG 1020  
Bgl II 978 9 +1 101 102 107 108  
CTCCCAGGTG CACGATGTA TGGTACCAAG GTGGAAATCA AAGCTACGGT GGCTGCACCA 1080  
1038 9 1062 3 Bsi VI  
TCTGTCTTCA TCTTCCCGCC ATCTGATGAG CAGTTGAAAT CTGGAATGCT CTCTGTTGTG 1140  
TGCTGCTGA ATAACCTCTA TCCAGAGAG GCCAAAGTAC AGTGAAGGT GGATAACGCC 1200  
HUMAN KAPPA CONSTANT 324bp 107 AMINO ACID & STOP CODON  
CTCCAATCGG GTAACCTCCA GGAGAGTGTC ACAGAGCAGG ACAGCAAGGA CAGCACCTAC 1260  
AGCCTCAGCA GCACCCTGAC GCTGAGCAA GCAGACTACG AGAAACACAA AGTCTACGCC 1320  
TGGGAAGTCA CCCATCAGGG CCTGAGCTCG CCCGTCACAA AGAGCTTCAA CAGGGGAGAG 1380  
STOP  
LIGHT CHAIN Eco RI LINKER #4=85bp  
TGTTCAATTC AGATCCGTTA ACGGTTACCA ACTACCTAGA CTGGATTCTG GACAACATGC 1440  
1386 7 1471 2  
GGCCGTGATA TCTACGTATG ATCAGCCTCG ACTGTGCTT CTAGTTGCCA GCCATCTGTT 1500

FIG. 2A

GTTTGCCCT CCCCGTGCC TTCCTTGACC CTGGAAGGTG CCACTCCCAC TGTCTTTCC 1560  
 TAATAAAATG AGGAAATTGC **BGH poly A=231bp** ATCGCATTGT CTGAGTAGGT GTCATTCTAT TCTGGGGGGT 1620  
 GGGGTGGGGC AGGACAGCAA GGGGGAGGAT TGGGAAGACA ATAGCAGGCA TGCTGGGGAT 1680  
 GCGGTGGGCT CTATGGAACC **LINKER #5=15bp** | ACCTGGGGCT CGACAGCTAT GCCAAGTACG CCCCCTATTG 1740  
 1702<sup>3</sup> 1717<sup>8</sup>  
 ACGTCAATGA CGGTAAATGG CCCGCCTGGC ATTATGCCCA GTACATGACC TTATGGGACT 1800  
 TTCTACTTG GCAGTACATC TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGTTTT 1860  
 GGCAGTACAT CAATGGGCGT **CMV PROMOTER-ENHANCER=334bp** GGATAGCGGT TTGACTCACG GGGATTTCAC AGTCTCCACC 1920  
 CCATTGACGT CAATGGGAGT TTGTTTTGGC ACCAAAATCA ACGGAGCTTT CAAAATGTC 1980  
 GTAACAACCT CGCCCCATTG ACGCAAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTATA 2040  
 TAAGCAGAGC **LINKER #6=7bp** TGGGTACGTC CTCACATTCA GTGATCAGCA CTGAACACAG **Sal I** ACCGTCGCAC 2100  
 2051<sup>2</sup> 2058<sup>9</sup> **LEADER=51bp** **Mlu I 2151** **Nhe I**  
 ATCGGTGGGA GCCTCATCTT GCTCTTCCTT GTCGCTGTTG **CTACGCGTGT** **CGCTAGCACC** 2160  
**START HEAVY CHAIN** -5 -4 -3 114 115  
 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACACCG 2220  
 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACCTCA 2280  
 GCGGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 2340  
 TCCTCTAGCA GCGTGGTGAC **HUMAN GAMMA 1 CONSTANT** CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 2400  
**993bp=330 AMINO ACID & STOP CODON**  
 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGCAGAGCC CAAATCTTGT 2460  
 GACAAAACCT ACACATGCCC ACCGTGCCCC GCACCTGAAC TCCTGGGGGG ACCGTCACTC 2520  
 TTCTCTTCC CCCCCAAACC CAAGGACACC CTCATGATCT CCGGACCCCT TGAGGTCACTA 2580  
 TGGTGGTGTT TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC 2640  
 GCGGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC 2700  
 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGACTACAAAG 2760  
 TGCAAGGTCT CCAACAAGAC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA 2820  
 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCGGGATGA GCTGACCAGG 2880  
 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG 2940  
 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC 3000

FIG. 2B

GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG 3060  
 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC 3120  
 STOP HEAVY CHAIN | Bam HI LINKER #7=81bp  
 CTCTCCCTGT CTCGGGTAA ATCAGGATCC GTTAACGGTT ACCAACTACC TAGACTGGAT 3180  
 TCGTGACAAC ATCGGGCCGT GATATCTACG TATGATCAGC CTCGACTGTG CCTTCTAGTT 3240  
 GCCAGCCATC TGTGTTTGC CCTCCCCCGG TGCTTCCTT GACCCTGGAA GGTGCCACTC 3300  
 BOVINE GROWTH HORMONE POLYADENYLATION REGION=231bp  
 CCACTGTCTT TCCTAATAA AATGAGGAAA TTGCATCGCA TTGTCTGAGT AGGTGTCATT 3360  
 CTATTCTGGG GGGTGGGGTG GGGCAGGACA GCAAGGGGGA GGTATTGGAA GACAATACCA 3420  
 GGCATGCTGG GGATGCGGTG GGCTCTATGG AACCAGCTGG 3480  
 LINKER #8=34bp  
 CCGCATCCCC 3490 AGCTTTGCTT CTCAATTCTT TATTTCGATA ATGAGAAAAA AAGGAAAATT 3540  
 AATTTTAACA CCAATTCAGT AGTTGATTGA GCAAATGCGT TGCCAAAAAG GATGCTTTAG 3600  
 MOUSE BETA GLOBIN MAJOR PROMOTER=366bp  
 AGACAGTGTT CTCTGCACAG AATAGGACAA ACATTATTCA GAGGGAGTAC CACAGAGTGA 3660  
 GACTCCTAAG CCAGTGAGTG GCACAGCATT CTAGGGAGAA ATATGCTTGT CATCACCGAA 3720  
 GCCTGATTCC GTAGAGCCAC ACCTTGGTAA GGGCCAATCT GCTCACACAG GATAGAGAGG 3780  
 GCAGGAGCCA GGGCAGAGCA TATAAGGTGA GGTAGGATCA GTTGCTCCTC ACATTTGCTT 3840  
 LINKER #9=19bp 5' UNTRANSLATED DHFR=82bp  
 CTGACATAGT TGTGTTGGGA GCTTGGATAG CTGGACAGC TCAGGGCTGC GATTTTCGCG 3900  
 CAAACTTGAC GGCAATCCTA GCGTGAAGGC TGGTAGGATT TTATCCCCGC TCCCATCAT 3960  
 START DHFR 3957  
 GTTCGACCAT TGAAGTGCAT CGTCGCCGTG TCCCAAAATA TGGGGATTGG CAAGAACGGA 4020  
 GACCTACCTT GGCCTCCGCT CAGGAACGAG TTCAAGTACT TCCAAAGAAT GACCACAACC 4080  
 TCTTCAGTGG AAGGTAACA GAATCTGGTG ATTATGGGTA GGAAAAACCTG GTTCTCCATT 4140  
 MOUSE DHFR=564bp=187 AMINO ACID & STOP CODON  
 CCTGAGAAAG ATCGACCTTT AAAGGACAGA ATTAATATAG TTCTCAGTAG AGAACTCAAA 4200  
 GAACCAACCAC GAGGAGCTCA TTTTCTTGCC AAAAGTTTGG ATGATGCCCT AAGACTTATT 4260  
 GAACAACCGG AATTGGCAAG TAAAGTAGAC ATGTTTGGGA TAGTCGGAGG CAGTTCTGTT 4320  
 TACCAGGAAG CCATGAATCA ACCAGGCCAC CTAGACTCT TTGTGACAAG GATCATGCAG 4380  
 GAATTTGAAA GTGACACGTT TTTCCAGAA ATTGATTTGG GGAATATATA ACTTCTCCCA 4440  
 GAATACCCAG GCGTCTCTCT TGAGGTCCAG GAGGAAAAAG GCATCAAGTA TAAGTTTGAA 4500

FIG. 2C

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STOP DHFR  
 GTCTACGAGA AGAAAGAC<sup>4521</sup>TA ACAGGAAGAT GCTTTCAAGT TCTCTGCTCC C<sup>4521</sup>CTCCTAAAG 4560  
 3' UNTRANSLATED DHFR=82bp [LINKER #10=10bp]  
 TCATGCATTT TTATAAGACC ATGGGACTTT TGCTGGCTTT AGATCAGCCT CGACTGTGCC 4620  
 4603 4 4613 4  
 TTCTAGTTGC CAGCCATCTG TTGTTTGCCC CTC<sup>4603</sup>CCCCGTG CCTTCCTTGA CCCTGGAAGG 4680  
 BOVINE GROWTH HORMONE POLYADENYLATION REGION=231bp  
 TGCCACTCCC ACTGTCCCTT CCTAATAAAA TGAGGAAATT GCATCGCATT GTCTGAGTAG 4740  
 GTGTCTATTCT ATTCTGGGGG GTGGGGTGGG GCAGGACAGC AAGGGGGAGG ATTGGGAAGA 4800  
 CAATAGCAGG CATGCTGGGG ATGCGGTGGG CTCTATGGAA CCAGCTGGGG CTCGAGCTAC 4860  
 4844 5 [LINKER #11=17bp]  
 TAGCTTTGCT TCTCAATTC TTATTGTCAT AATGAGAAAA AAAGGAAAT TAATTTTAAAC 4920  
 ACCAATTCAG TAGTGTATTG AGCAAATGCG TTGCCAAAAA GGATGCTTTA GAGACAGTGT 4980  
 MOUSE BETA GLOBIN MAJOR PROMOTER=366bp  
 TCTCTGCACA GATAAGGACA AACATTATTC AGAGGGAGTA CCCAGAGCTG AGACTCCTAA 5040  
 GCCAGTGAGT GGCACAGCAT TCTAGGGAGA AATATGCTTG TCATCACCGA AGCCTGATTG 5100  
 CGTAGAGCCA CACCTTGGTA AGGGCCAATC TGCTCACACA GGATAGAGAG GGCAGGAGCC 5160  
 AGGGCAGAGC ATATAAGGTG AGGTAGGATC AGTTGCTCCT CACATTGCT TCTGACATAG 5220  
 [LINKER #12=21bp] [START NEO]  
 TTGTGTTGGG AGCTTGGATC GATCCTCTAT GGTGAACAA GATGGATTGC ACGCAGGTTC 5280  
 5227 8 5248 9  
 TCCGGCCGCT TGGGTGGAGA GGCTATTCCG CTATGACTGG GCACAACAGA CAATCGGCTG 5340  
 CTCTGATGCC GCCGTGTTCC GGCTGTGAGC GCAGGGGGCG CCGGTTCTTT TTGTCAAGAC 5400  
 NEOMYCIN PHOSPHOTRANSFERASE  
 CGACCTGTCC GGTGCCCTGA ATGAACTGCA GGACGAGGCA CGCGGGCTAT CGTGCGTGGC 5460  
 795bp=264 AMINO ACIDS & STOP CODON  
 CACGACGGGC GTTCCTTGGC CAGCTGTGCT CGACGTTGTC ACTGAAGCGG GAAGGGACTG 5520  
 GCTGCTATTG GCGGAAGTGC CGGGGCAGGA TCTCTGTCA TCTACCTTG CTCTGCGCGA 5580  
 GAAAGTATCC ATCATGGGTG ATGCAATGCG GCGGCTGCAT ACGCTTGATC CGGCTACCTG 5640  
 CCCATTGAC CACCAAGCGA AACATCGCAT CGAGCGAGCA CGTACTCGGA TGAAGCCGG 5700  
 TCTTGTCGAT CAGGATGATC TGGACGAAGA GCATCAGGGG CTCGCGCCAG CCGAACTGTT 5760  
 CGCCAGGCTC AAGGCGCGCA TGCCCGACGG CGAGGATCTC GTCGTGACC ATGGCGATGC 5820  
 CTGCTTGGCG AATATCATGG TGGAAAAATG CCGCTTTTCT GGATTCATCG ACTGTGGCCG 5880  
 GCTGGGTGTG GCGGACCGCT ATCAGGACAT AGCGTTGGCT ACCCGTGATA TTGCTGAAGA 5940  
 GCTTGGCGGC GAATGGGCTG ACCGCTTCCT CGTGCTTTAC GGTATCGCGG CTCCCGGATC 6000

FIG. 2D

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GCAGCGCATC GCCTTCTATC GCCTTCTTGA CGAGTTCCTC <sup>STOP NEO</sup>TCAGCGGGAC TCTGGGGTTC 6060  
 604314  
 GAAATGACCG ACCAAGCGAC GCCCAACCTG CCATCAGGAG ATTTCCGATTC CACCGCCGCC 6120  
 3' UNTRANSLATED NEO=173bp  
 TTCTATGAAA GGTGTGGGCTT CGGAATCGTT TTCGGGGACG CCGGCTGGAT GATCCTCCAG 6180  
 CGCGGGGATC TCATGCTGGA GTTCTTCGCC CACCCCACT TGTATTATGC AGCTTATAAT 6240  
 621617  
 GGTACAAAT AAAGCAATAG CATCACAAT TTCACAAATA AAGCATTTTT TCACTGCAT 6300  
 SV40 POLY A EARLY=133bp LINKER #13=19bp  
 TCTAGTTGTG GTTTGTCCAA ACTCATCAAT CTATCTTATC ATGTCCTGAT CGCGGCCGCG 6360  
 6349150  
 ATCCCGTCCA GAGCTTGGCG TAATCATGGT CATAGCTGTT TCCTGTGTGA AATTGTTATC 6420  
 636819  
 CGCTCACAAT TCCACACAAC ATACGAGCGG GAAGCATAAA GTGTAAAGCC TGGGGTGCCT 6480  
 AATGAGTGAG CTAAGTCACA TTAATTGCGT TCGCTCACT GCCCGCTTTC CAGTCGGGAA 6540  
 ACCTGTCGTG CCAGCTGCAT TAATGAATCG GCCAACGCGC GGGGAGAGGC GGTTTGCGTA 6600  
 TTGGGCGCTC TTCGCTTCC TCGCTCACTG ACTCGCTGCG CTCGGTCGTT CGGCTGCGGC 6660  
 PVC 19  
 GAGCGGTATC AGCTCACTCA AAGGCGGTAA TACGTTATC CACAGAATCA GGGGATAACG 6720  
 CAGGAAAGAA CATGTGAGCA AAAGGCCAGC AAAAGGCCAG GAACCGTAAA AAGGCCGCGT 6780  
 6792=BACTERIAL ORIGIN OF REPLICATION  
 TGCTGGCGTT TTTCCATAGG CTCCGCCCCC CTGACGAGCA TCACAAAAAT CGACGCTCAA 6840  
 GTCAGAGGTG GCGAAACCCG ACAGGACTAT AAAGATACCA GCGGTTTCCC CCTGGAAGCT 6900  
 CCCTCGTGCG CTCTCTGTT CCGACCCGTC CGCTTACCGG ATACCTGTCC GCCTTCTCC 6960  
 CTTCGGGAAG CGTGGCGCTT TCTCAATGCT CACGCTGTAG GTATCTCAGT TCGGTGTAGG 7020  
 TCGTTGCGTC CAAGCTGGGC TGTGTGCACG AACCCCGCT TCAGCCCGAC CGCTGCGCCT 7080  
 TATCCGGTAA CTATCGTCTT GAGTCCAACC CGGTAAGACA CGACTTATCG CCACTGGCAG 7140  
 CAGCCACTGG TAACAGGATT AGCAGAGCGA GGTATGTAGG CGGTGCTACA GAGTCTTGA 7200  
 AGTGGTGGCC TAAGTACGGC TACACTAGAA GGACAGTATT TGGTATCTGC GCTCTGCTGA 7260  
 AGCCAGTTAC CTTCCGAAAA AGAGTTGGTA GCTCTTGATC CGGCAACAA ACCACCGCTG 7320  
 GTAGCGGTGG TTTTGTGTT TGCAAGCAGC AGATTACGCG CAGAAAAAAA GGATCTCAAG 7380  
 AAGATCCTTT GATCTTTTCT ACGGGGTCTG ACGCTCAGTG GAACGAAAAA TCACGTTAAG 7440  
 GGATTTTGGT CATGAGATTA TCAAAAAGGA TCTTCACCTA GATCCTTTTA AATTAATAAT 7500

FIG. 2E

GAAGTTTTAA ATCAATCTAA AGTATATATG AGTAAACTTG GTCTGACAGT TACCAATGCT 7560  
 TAATCAGTGA GGCACCTATC TCAGCGATCT GTCTATTTTCG TTCATCCATA GTTGCCCTGAC 7620  
 TCCCGGTCGT GTAGATAACT ACGATACGGG AGGGCTTACC ATCTGGCCCC AGTGCTGCAA 7680  
 TGATACCGCG AGACCCACGC TCACCGGCTC CAGATTTATC AGCAATAAAC CAGCCAGCCG 7740  
 GAAGGGCCGA GCGCAGAAGT GGTCCCTGCAA CTTTATCCGC CTCCATCCAG TCTATTAATT 7800  
 GTTGCCCGGA AGCTAGAGTA AGTAGTTCGC CAGTTAATAG TTTGCGCAAC GTTGTTGCCA 7860  
 TTGCTACAGG CATCGTGGTG TCACGCTCGT CGTTTGGTAT GGCTTCATTC AGTCCGGTT 7920  
 CCCAACGATC AAGGCGAGTT ACATGATCCC CCATGTTGTG CAAAAAGCG GTTAGCTCCT 7980  
 TCGGTCTCC GATCGTTGTC AGAAGTAAGT TGGCCGCAGT GTTATCACTC ATGGTTATGG 8040  
 CAGCACTGCA TAATTCTCTT ACTGTCAATG CATCCGTAAG ATGCTTTTCT GTGACTGGTG 8100  
 AGTACTCAAC CAAGTCATTC TGAGAATAGT GTATGCGGCG ACCGAGTTGC TCTTGCCCGG 8160  
 CGTCAATACG GGATAATACC GCGCCACATA GCAGAACTTT AAAAGTGCTC ATCATTGGAA 8220  
 AACGTTCTTC GGGGCGAAAA CTCTCAAGGA TCTTACCCTG GTTGAGATCC AGTTCGATGT 8280  
 AACCCTCTCG TGCACCCAAC TGATCTTCAG CATCTTTTAC TTTACCAGC GTTCTGGGT 8340  
 GAGCAAAAAC AGGAAGGCAA AATGCCGCAA AAAAGGGAAT AAGGGCGACA CGGAAATGTT 8400  
 GAATACTCAT ACTCTTCCTT TTTCAATATT ATTGAAGCAT TTATCAGGCT TATTGTCTCA 8460  
 TGAGCGGATA CATATTGAA TGTATTTAGA AAAATAAACA AATAGGGGTT CCGCGCACAT 8520  
 TTCCCGGAAA AGTGCCACCT

FIG. 2F

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LINKER #1=15bp  
GACGTCGCG CCGCTCTAGG CCTCCAAAA AGCCTCCTCA CTACTTCTGG AATAGCTCAG 50  
15'6

AGGCCGAGGC GGCCTCGGCC TCTGCATAAA TAAAAAAAT TAGTCAGCCA TGCATGGGGC 120

SV40 ORIGIN=332bp  
GGAGAATGGG CGGAAC TGGG CCGAGTTAGG GCGGGGATGG GCGGAGTTAG GGGCGGGACT 180

ATGGTTGCTG ACTAATTGAG ATGCATGCTT TGCATACTTC TGCTGCTGG GGAGCCTGGG 240

GACTTTCCAC ACCTGGTTGC TGACTAATTG AGATGCATGC TTTGCATACT TCTGCCTGCT 300

GGGGAGCCTG GGGACTTTCC ACACCC TAAC TGACACACAT TCCACAGAAT TAATTCCTCT 360  
LINKER #2=13bp  
347'8

AGTTATTAAT AGTAATCAAT TACGGGGTCA TTAGTTCATA GCCATATAT GGAGTTCGCG 420

GTTACATAAC TTACGGTAAA TGGCCCCGCT GGCTGACCGC CCAACGACCC CCGCCCATTTG 480

ACGTCAATAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA TTGACGTCAA 540

CVM PROMOTER-ENHANCER=567bp  
TGGGTGGACT ATTTACGGTA AACTGCCAC TTGGCAGTAC ATCAAGTGTA TCATATGCCA 600

AGTACGCCCC CTATTGACGT CAATGACGGT AAATGGCCCG CCTGGCATTG TGCCCGATAC 660

ATGACCTTAT GGGACTTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC 720

ATGGTGATGC GGTTTTGGCA GTACATCAAT GGGCGTGGAT AGCGGTTTGA CTCACGGGGA 780

TTTCCAAGTC TCCACCCCAT TGACGTCAAT GGGAGTTTGT TTTGGCACCA AAATCAACGG 840

GACTTTCCAA AATGTCGTAA CAACTCCGCC CCATTGACGC AAATGGCGCG TAGGCGTGTA 900

CGGTGGGAGG TCTATATAAG CAGAGCTGGG TACGTGAACC GTCAGATCGC CTGGAGACGC 960  
LINKER #3=7bp  
927'8 934'5

Bgl 2 START LIGHT CHAIN NATURAL LEADER=66bp  
CATCACAGAT CTCTCACTAT G GATTTCAG GTGCAGATTA TCAGCTTCCT GCTAATCAGT 1020  
978'9

GCTTCAGTCA TAATGTCCAG AGGACAAATT GTTCTCTCCC AGTCTCCAGC AATCCTGTCT 1080  
1044'5-1

GCATCTCCAG GGGAGAAGGT CACAATGACT TGCAGGGCCA GCTGAAGTGT AAGTTACATC 1140

CACTGGTTCC AGCAGAAGCC AGGATCCTCC CCCAAACCT GGATTTATGC CACATCCAAC 1200

LIGHT CHAIN VARIABLE REGION 318bp 106 AMINO ACID  
CTGGCTTCTG GAGTCCCTGT TCGCTTCAGT GGCAGTGGGT CTGGGACTTC TTACTCTCTC 1260

ACCATCAGCA GAGTGGAGGC TGAAGATGCT GCCACTTATT ACTGCCAGCA GTGGACTAGT 1320

AACCCACCCA CGTTCCGAGG GGGGACCAAG CTGGAAATCA AACGTACGGT GGCTGCACCA 1380  
BsiWI  
1362'3

TCTGTCTTCA TCTTCCCGCC ATCTGATGAG CAGTTGAAAT CTGGAAGTGC CTCTGTTGTG 1440

TGCCTGCTGA ATAACCTCTA TCCAGAGAG GCCAAAGTAC AGTGAAGGT GGATAACGCC 1500

FIG. 3A



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HUMAN KAPPA CONSTANT=324bp=107 AMINO ACID & STOP CODON  
 CTCCAATCGG GTAACCTCCA GGAGAGTGT ACAGAGCAGG ACAGCAAGGA CAGCACCTAC 1560  
 AGCCTCAGCA GCACCCTGAC GCTGAGCAAA GCAGACTACG AGAAACACAA AGTCTACGCC 1620  
 TCGGAAGTCA CCCATCAGGG CCTGAGCTCG CCCGTCACAA AGAGCTTCAA CAGGGGAGAG 1680  
 STOP  
 LIGHT CHAIN Eco RI LINKER #4=81bp  
 TGTGGAATTC AGATCCGTTA ACGGTTACCA ACTACCTAGA CTGGATTCGT GACAACA<sup>-</sup>GC 1740  
 1646<sup>1</sup>7  
 GGCCGTGATA TCTACGTATG ATCAGCCTCG ACTGTGCCTT CTAGTTGCCA GCCATCTGTT 1800  
 1771<sup>1</sup>2  
 GTTGGCCCT CCCCCGTGCC TTCCTTGACC CTGGAAGGTG CCACTCCAC TGCTCTTTC 1860  
 TAATAAATG AGGAAATTGC ATCGCATTGT CTGAGTAGGT GTCATTCTAT TCTGGGGGGT 1920  
 BOVINE GROWTH HORMONE POLYADENYLATION REGION=231bp  
 GGGGTGGGC AGGACAGCA GGGGAGGAT TGGGAAGACA ATAGCAGGCA TGCTGGGGAT 1980  
 GCGGTGGCT CTATGGAAC AGCTGGGGCT CGACAGCTAT GCCAAGTACG CCCCCTATTG 2040  
 2002<sup>1</sup>3 2017<sup>1</sup>8  
 ACGTCAATGA CGGTAATGG CCCGCCTGCC ATTATGCCA GTACATGACC TTATGGGACT 2100  
 TTCCTACTTG GCAGTACATC TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGTTTT 2160  
 CMV PROMOTER-ENHANCER=334bp  
 GGCAGTACAT CAATGGGCGT GGATAGCGGT TTGACTCAG GGGATTTCCA AGTCTCCACC 2220  
 CCATTGACGT CAATGGGAGT TTGTTTTGCC ACCAAATCA ACGGGACTTT CCAAAATGTC 2280  
 GTAACAACCT CGCCCCATTG ACGCAAATGG GCGGTAGCGG TGTACGGTGG GAGGTCTATA 2340  
 LINKER #6=7bp Sal I  
 TAAGCAGAGC TGGGTACGTC CTCACATTCA GTGATCAGCA CTGAACACAG ACCCGTCGAC 2400  
 START 2351<sup>1</sup>2 2358<sup>1</sup>9  
 HEAVY CHAIN SYNTHETIC & NATURAL LEADER Mlu I 2457<sup>1</sup>8  
 ATGGGTGGA GCCTCATCTT GCTCTTCTT GTGCGTGTG CTACGGGTGT CCTGTCCAG 2460  
 2401 -5 -4 -3 -2 -1 +1  
 GTACAACTGC AGCAGCCTGG GGCTGAGCTG GTGAAGCCTG GGGCCTCAGT GAAGATGTC 2520  
 TGCAAGGCTT CTGGCTACAC ATTTACCAGT TACAATATGC ACTGGGTAA ACAGACACCT 2580  
 HEAVY CHAIN VARIABLE=363bp=121 AMINO ACID  
 GGTGCGGGCC TGGAAATGGAT TGGAGCTATT TATCCCGGAA ATGGTGATAC TTCCTACAAT 2640  
 CAGAAGTTCA AAGGCAAGGC CACATTGACT GCAGACAAAT CCTCCAGCAC AGCCTACATG 2700  
 CAGCTCAGCA GCCTGACATC TGAGGACTCT GCGGTCTATT ACTGTGCAAG ATCGACTTAC 2760  
 TACGCGGTG ACTGGTACTT CAATGTCTGG GCGCAGGGA CCACGGTCAC CGTCTCTGC 2820  
 Nhe I  
 GCTAGCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCTT CCTCCAAGAG CACCTCTGGG 2880  
 GGCACAGCGG CCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCAGT GACGGTGTGG 2940  
 HUMAN GAMMA 1 CONSTANT=993bp  
 TGAAGCTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCTT ACAGTCTCTA 3000

FIG. 3B

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GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC 3960  
 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGCAGAGCCC 3120  
 AAATCTTGTG ACAAACCTCA CACATGCCCA CCGTGCCCAG CACCTGAACT CTTGGGGGGA 3180  
 CCGTCAGTCT TCCTCTTCCC CCCAAAACCC AAGGACACCC TCATGATCTC CCGGACCCCT 3240  
 GAGGTCACAT GCGTGGTGGT GGACGTGAGC CACGAAGACC CTGAGGTCAA GTTCAACTGG 3300  
 TACGTGGAGC GCGTGGAGGT GCATAATGCC AAGACAAAGC CGCGGGAGGA GCAGTACAA 3360  
 AGCACGTACC GTGTGGTCAG CGTCTCACC GTCTGCACC AGGACTGGCT GAATGGCAAG 3420  
 GAGTACAAGT GCAAGGTCTC CAACAAAGCC CTCCCAGCCC CCATCGAGAA AACCATCTCC 3480  
 AAAGCCAAAG GGCAGCCCCG AGAACCACAG GTGTACACCC TGCCCCCCTC CCGGGATGAG 3540  
 CTGACCAAGA ACCAGGTGAG CCGTACCTGC CTGGTCAAAG GCTTCTATCC CAGCGACATC 3600  
 GCCGTGGAGT GGGAGAGCAA TGGGCGAGCCG GAGAACAAC TACAAGACCAC GCCTCCCGTG 3660  
 CTGGACTCCG ACGGCTCCTT CTCTCTTAC AGCAAGCTCA CCGTGACAA GAGCAGGTGG 3720  
 CAGCAGGGGA ACGTCTTCTC ATGCTCCGTG ATGCATGAG CTCTGCACAA CCACTACACG 3780  
 CAGAAGAGCC TCTCCCTGTC TCCGGGTAAA TGAGGATCCG TTAACGGTTA CCAACTACCT 3840  
 AGACTGGATT CGTGACAACA TCGGGCCGTG ATATCTACGT ATGATCAGCC TCGACTGTGC 3900  
 CTCTAGTTG CCAGCCATCT GTTGTGTTGCC CCTCCCCCGT GCCTTCTCTG ACCCTGGAG 3960  
 GTGCCACTCC CACTGTCTT TCCTAATAAA ATGAGGAAAT TGCATCGCAT TGTCTGAGTA 4020  
 GGTGTCAATC TATTCTGGG GGTGGGGTGG GGCAGGACAG CAAGGGGGAG GATTGGGAAG 4080  
 ACAATAGCAG GCATGCTGGG GATGCGGTGG GCTCTATGGA ACCAGCTGGG GCTCGACAGC 4140  
 GCTGGATCTC CCGATCCCCA GCTTTGCTTC TCAATTTCTT ATTTGCATA TTAGAAAAAA 4200  
 AGGAAATTA ATTTAACAC CAATTCAGTA GTTGATTGAG CAAATGCGTT GCCAAAAAGG 4260  
 ATGCTTTAGA GACAGTGGT TCTGCACAGA TAAGGACAAA CATTATTCAG AGGGAGTACC 4320  
 CAGAGCTGAG ACTCCTAAGC CAGTGAGTGG CACAGCATTC TAGGGAGAAA TATGCTGTGC 4380  
 ATCACCAGAG CCTGATTCCG TAGAGCCACA CCTTGGTAAG GGCCAATCTG CTCACACAG 4440  
 ATAGAGAGGG CAGGAGCCAG GGCAGAGCAT ATAAGGTGAG GTAGGATCAG TTGCTCTCA 4500

FIG. 3C

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CATTTCCTTC TGACATAGTT LINKER #9=19bp 5' UNTRANSLATED DHFR=82bp  
 TGTTCGGAG CTTCGATAGC TTGGACAGCT CAGGGCTCGG 4560  
 4525 8 4544 5  
 ATTTCGCGCC AAACCTTGACG GCAATCCTAG CGTGAAGGCT GGTAGGATTT TATCCCCGCT 4620  
START DHFR  
 GCCATCATGG TTCCGACCATT GAACCTGCATC GTCGCCGTGT CCCAAAATAT GGGGATTGGC 4680  
 4626 7  
 AAGAACGGAG ACCTACCCCTG GCCTCCGCTC AGGAACGAGT TCAAGTACTT CCAAAGAATG 4740  
 ACCACAACCT CTTCAGTGGG AGGTAAACAG AATCTGGTGA TTATGGGTAG GAAAACCTGG 4800  
DHFR=564bp=187 AMINO ACID & STOP CODON  
 TTCTCCATTC CTGAGAAGAA TCGACCTTTA AAGGACAGAA TTAATATAGT TCTCAGTAGA 4860  
 GAACCTCAAG AACCACCACG AGGAGCTCAT TTTCTTGCCA AAAGTTTGGA TGATGCCTTA 4920  
 AGACTTATTG AACAAACCGGA ATTGGCAAGT AAAGTAGACA TGGTTTGGAT AGTCGGAGGC 4980  
 AGTTCTGTTT ACCAGGAAGC CATGAATCAA CCAGGCCACC TTAGACTCTT TGTGACAAGG 5040  
 ATCATGCGAG AATTTGAAAG TGACACGTTT TTCCAGAAA TTGATTTGGG GAAATATAAA 5100  
 CTTCTCCCAG AATACCCAGG CGTCTCTCTT GAGGTCCAGG AGGAAAAAGG CATCAAGTAT 5160  
STOP DHFR 3' UNTRANSLATED DHFR=82bp  
 AAGTTTGAAG TCTACGAGAA GAAAGACTAA CAGGAAGATG CTTTCAAGTT CTCTGCTCCC 5220  
 5140 1  
 CTCCTAAAGC TATGCATTTT TATAAGACCA TGGGACTTTT GCTGGCTTTA LINKER #10  
 =10bp GATCAGCCTC 5272 3  
 GACTGTGCGCT TCTAGTTGCC AGCCATCTGT TGTTTGCCCC TCCCCGTGC CTTCCTTGAC 5340  
BOVINE GROWTH HORMONE POLYADENYLATION=231bp  
 CCTGGAAGGT GCCACTCCCA CTGCTCTTTC CTAATAAAAT GAGGAAATTG CATCGCATTTG 5400  
 TCTGAGTAGG TGTCATTCTA TTCTGGGGGG TGGGGTGGGG CAGGACAGCA AGGGGGAGGA 5460  
LINKER #11  
 TTGGGAAGAC AATAGCAGGC ATGCTGGGGA TGCGGTGGGC TCTATGGAAC CAGCTGGGGC 5520  
 5513 4  
 =17bp TCGAGCTACT AGCTTTGCTT CTCAATTTCT TATTTGCATA ATGAGAAAAA AAGGAAAAAT 5580  
 5530 1  
MOUSE BETA GLOBIN MAJOR PROMOTER=368bp  
 AGACAGTGT CTCTGCACAG ATAAGGACAA TAGGGAGAA ATATGCTTGT CATCACCGAA 5700  
 GACTCCTAAG CCAGTGAGTG GCACAGCATT CTAGGGAGAA ATATGCTTGT CATCACCGAA 5760  
 GCCTGATTCC GTAGAGCCAC ACCTTGGTAA GGGCCAATCT GCTCACACAG GATAGAGAGG 5820  
 GCAGAGGCCA GGGCAGAGCA TATAAGGTGA GGTAGGATCA GTTGCTCCTC ACATTTGCTT 5880  
LINKER #12=21bp START NEO  
 CTGACATAGT TGTGTTGGG GCTTGGATCG ATCCTCTATG GTTGAACAAG ATGGATTGCA 5940  
 5896 7 5917 8  
 CGCAGGTTCT CCGGCCGCTT GGTGGGAGAG GCTATTCTGC TATGACTGGG CACAACAGAG 6000

FIG. 3D

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AATCGGCTGC TCTGATGCCG CCGTGTTCGG GCTGTCAGCG CAGGGGGCGC CGGTCTCTTT 6060  
**NEOMYCIN PHOSPHOTRANSFERASE=795bp=264 AMINO ACID & STOP CODON**  
 TGTCAGAGCC GACCTGTCCG GTGCCCTGAA TGAACCTGCAG GACGAGGCAG CGCGGCTATC 6120  
 GTGGCTGGCC ACGACGGGCG TTCTTGGCGC AGCTGTGCTC GACGTTGTCA CTGAAGCGGG 6180  
 AAGGGACTGG CTGTATTGG GCGAAGTGCC GGGGCAGGAT CTCCTGTGAT CTCACCTTGC 6240  
 TCCTGCCGAG AAAGTATCCA TCATGGCTGA TGCAATGCGG CGGCTGCATA CGCTTGATCC 6300  
 GGCTACCTGC CCATTGAGCC ACCAAGCGAA ACATCGCATC GAGCGAGCAC GTACTCGGAT 6360  
 GGAAGCCGGT CTTGTGATC AGGATGATCT GGACGAAGAG CATCAGGGGC TCGGCCAGCG 6420  
 CGAACTGTC GCCAGGCTCA AGGCGCGCAT GCCGACGGC GAGGATCTCG TCGTGACCCA 6480  
 TGCGCATGCC TGCTTGCCGA ATATCATGGT GGAAAATGGC CGCTTTTCTG GATTTCATGA 6540  
 CTGTGGCCGG CTGGGTGTGG CGGACCGCTA TCAGGACATA GCGTTGGCTA CCCGTGATAT 6600  
 TGCTGAAGAG CTTGGCGGGC AATGGGCTGA CGGCTTCCTC GTGCTTTATG GTATCGCGCT 6660  
 TCCCGATTGC CAGCGCATCG CCTTCTATCG CCTTCTTGAC **STOP NEO** 6720  
 CTGGGGTTGC AAATGACCGA CCAAGCGAGC CCCAACCTGC CATCAGGAGA TTTCGATTCC 6780  
**3' UNTRANSLATED NEO=173bp**  
 ACCGCCGCCCT TCTATGAAAG GTTGGGCTTC GGAATCGTTT TCCGGGACGC CGGCTGGATG 6840  
 ATCTCCAGC GCGGGGATCT CATGCTGGAG TTCTTCGCTC ACCCGAACCT GTTTATTGCA 6900  
 GCTTATAATG GTTACAAATA AAGCAATAGC ATCACAATTT TCACAAATAA AGCATTTTTT 6960  
**SV40 EARLY POLYADENYLATION REGION=133bp**  
 TCACTGCATT CTAGTTGTGG TTGTGCTCAA CTCATCAATC TATCTTATCA TGTCTGGATC 7020  
**LINKER #13=19bp**  
 GCGGCCGCGA TCCCGTCCAG AGCTTGGCGT AATCATGGTC ATAGCTGTTT CCTGTGTGAA 7080  
**PUC 19**  
 ATTGTTATCC GCTCACAATT CCACACAACA TACGAGCCGG AAGCATAAAG TGTAAGCTCT 7140  
 GGGGTGCCTA ATGAGTGAGC TAACTCACAT TAATTGCGTT GCGCTCACTG CCCGCTTTCC 7200  
 AGTCGGGAAA CCTGTCGTGC CAGCTGCATT AATGAATCGG CCAACGCGCG GGGAGAGGCG 7260  
 GTTTGCGTAT TGGGCGCTCT TCCGCTTCCT CGCTCACTGA CTCGCTGCGC TCGGTCGTTT 7320  
 GGCTGCGGCG AGCGGTATCA GCTCACTCAA AGGCGGTAAT ACGGTTATCC ACAGAAATCA 7380  
 GGGATAACGC AGGAAAGAAC ATGTGAGCAA AAGGCCAGCA AAAGGCCAAG AACCGTAAAA 7440  
**7461=BACTERIAL ORIGIN OF REPLICATION**  
 AGGCCGCGTT GCTGGCGTTT TTCCATAGGC TCCGCCCCCC TGACGAGCAT CACAAAAATC 7500

FIG. 3E

GACGCTCAAG TCAGAGGTGG CGAAACCCGA CAGGACTATA AAGATACCAG GCGTTTCCCC 7560  
 CTGGAAGCTC CCTCGTGC GC TCTCCTGTTT CGACCCTGCC GCTTACCGGA TACCTGTCCG 7620  
 CCTTTCTCCC TTCGGGAAGC GTGGCGCTTT CTCAATGCTC ACGCTGTAGG TATCTCAGTT 7680  
 CGGTGTAGGT CGTTCGCTCC AAGCTGGGCT GTGTGCACGA ACCCCCCGTT CAGCCCGACC 7740  
 GCTGCGCCTT ATCCGGTAAC TATCGTCTTG AGTCCAACCC GGTAAGACAC GACTTATCGC 7800  
 CACTGGCAGC AGCCACTGGT AACAGGATTA GCAGAGCGAG GTATGTAGGC GGTGCTACAG 7860  
 AGTTCTTGAA GTGGTGGCCT AACTACGGCT ACACTAGAAG GACAGTATTT GGTATCTGCG 7920  
 CTCTGCTGAA GCCAGTTACC TTCGGA AAAA GAGTTGGTAG CTCTTGATCC GGCAAAACAAA 7980  
 CCACCGCTGG TAGCGGTGGT TTTTTTGTTC GCAAGCAGCA GATTACGCGC AGAAAAAAG 8040  
 GATCTCAAGA AGATCCTTTG ATCTTTTCTA CGGGGTCTGA CGCTCAGTGG AACGAAAACT 8100  
 CACGTTAAGG GATTTTGTGC ATGAGATTAT CAAAAAGGAT CTTCACCTAG ATCCTTTTAA 8160  
 ATTA AAAATG AAGTTTAAA TCAATCTAAA GTATATATGA GTAAACTTGG TCTGACAGTT 8220  
BETA LACTAMASE  
 ACCAATGCTT AATCAGTGAG GCACCTATCT CAGCGATCTG TCTATTTCTG TCATCCATAG 8280  
 TTGCTGACT CCCCGTCTGT TAGATACTA CGATACGGGA GGGCTTACCA TCTGGCCCCA 8340  
 GTGCTGCAAT GATACCGCGA GACCCACGCT CACCGGCTCC AGATTATCA GCAATAAAC 8400  
 BETA LACTAMASE=861bp=286 AMINO ACID & STOP CODON  
 AGCCAGCCGG AAGGGCCGAG CGCAGAAGTG GTCCTGCAAC TTTATCCGCC TCCATCCAGT 8460  
 CTATTAATTG TTGCCGGGAA GCTAGAGTAA GTAGTTGCC AGTTAATAGT TTGCGCAACG 8520  
 TTGTTGCCAT TGCTACAGGC ATCGTGGTGT CACGCTCGTC GTTTGGTATG GCTTCATTCA 8580  
 GCTCCGGTTC CCAACGATCA AGCGAGTTA CATGATCCCC CATGTTGTGC AAAAAAGCGG 8640  
 TTAGCTCCTT CGGTCTCTCG ATCGTTGTCA GAAGTAAGTT GGCCGCACTG TTATCACTCA 8700  
 TGGTTATGGC AGCACTGCAT AATTCTCTTA CTGTCATGCC ATCCGTAAGA TGCTTTTCTG 8760  
 TGACTGGTGA GACTCAACC AAGTCATTCT GAGAATAGTG TATGCGGCGA CCGAGTTGCT 8820  
 CTTGCCCGGC GTCAATACGG GATAATACCG CGCCACATAG CAGAACTTTA AAAGTGCTCA 8880  
 TCATTGGAAA ACGTTCTTCG GGGCGAAAAA TCTCAAGGAT CTTACCGCTG TTGAGATCCA 8940  
 GGTGATGTGA ACCCACTCGT GCACCCAACAT GATCTTCAGC ATCTTTTACT TTCACCAGCG 9000  
 TTTCTGGGTG AGCAAAAAA GGAAGGCAAA ATGCCGCAAA AAAGGGAATA AGGGCGACAC 9060  
 GGAAATGTTG AATACTCAT START BETA LACTAMASE  
 CTCTTCCCTT TTCAATATTA TTGAAGCATT TATCAGGGTT 9120  
 ATTGTCTCAT GAGCGGATAC ATATTTGAAT GTATTTAGAA AAATAACAA ATAGGGGTTC 9180  
 CGCGCACATT TCCCCGAAAA GTGCCACCT

FIG. 3F

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## LEADER

FRAME 1 Met Asp Phe Gln Val Gln Ile Ile Ser Phe Leu Leu Ile Ser Ala Ser Val  
 ATG GAT TTT CAG GTG CAG ATT ATC AGC TTC CTG CTA ATC AGT GCT TCA GTC  
 987 996 1005 1014 1023

-5 Ile Met Ser Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser  
 ATA ATG TCC AGA GGA CAA ATT GTT CTC TCC CAG TCT CCA GCA ATC CTG TCT GCA TCT  
 1038 1047 1056 1065 1074 1083

20 23 24 CDR1 27 29 30 34  
 Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Ile His  
 CCA GGG GAG AAG GTC ACA ATG ACT TGC AGG GCC AGC TCA AGT GTA AGT TAC ATC CAC  
 1095 1104 1113 1122 1179 1188 1197

35 FR2 40 45 49 50 CDR2  
 Trp Phe Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn  
 TGG TTC CAG CAG AAG CCA GGA TCC TCC CCC AAA CCC TGG ATT TAT GCC ACA TCC AAC  
 1152 1161 1170 1179 1188 1197

55 56 57 60 FR3 65 70  
 Leu Ala Ser Gly Val Pro Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser  
 CTG GCT TCT GGA GTC CCT GTT CGC TTC AGT GGC AGT GGG TCT GGG ACT TCT TAC TCT  
 1209 1218 1227 1235 1245 1254

75 80 85 88 89 90  
 Leu Thr Ile Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
 CTC ACC ATC AGC AGA GTG GAG GCT GAA GAT GCT GCC ACT TAT TAC TGC CAG CAG TGG  
 1266 1275 1284 1293 1302 1311

CDR3 95 97 98 100 FR4 105 107  
 Thr Ser Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
 ACT AGT AAC CCA CCC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATC AAA  
 1323 1332 1341 1350 1359

FIG. 4

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## LEADER

-19										-15										-10										-5									
FRAME 1	Met	Gly	Trp	Ser	Leu	Ile	Leu	Leu	Phe	Leu	Val	Ala	Val	Ala	Thr	Arg	Val	ATG	GGT	TGG	AGC	CTC	ATC	TTG	CTC	TTC	CTT	GTC	GCT	GTT	GCT	ACG	CGT	GTC					
																		2409								2427					2436			2445					
-1										FR1										10										15									
Leu	Ser	Gln	Val	Gln	Leu	Gln	Gln	Pro	Gly	Ala	Glu	Leu	Val	Lys	Ala	Gly	Ala	Ser	CAG	GTA	CAA	CTG	CAG	CAG	CCT	GGG	GCT	GAG	CTG	GTG	AAG	CCT	GGG	GCC	TCA				
																			2460													2496			2505				
20										25										30										31 CDR1 35 36									
Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr	Asn	Met	His	Trp	GTG	AAG	ATG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACA	TTT	ACC	AGT	TAC	AAT	ATG	CAC	TGG		
																			2517																2562				
40 FR2										45										49										50 52 52A 53 54									
Val	Lys	Gln	Thr	Pro	Gly	Arg	Gly	Leu	Glu	Trp	Ile	Gly	Ala	Ile	Tyr	Pro	Gly	Asn	GTA	AAA	CAG	ACA	CCT	GGT	CGG	GGC	CTG	GAA	TGG	ATT	GGA	GCT	ATT	TAT	CCC	GGA	AAT		
																			2574																2610		2619		
55 CDR2 60										65										66 FR3 70																			
Gly	Asp	Thr	Ser	Tyr	Asn	Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	GGT	GAT	ACT	TCC	TAC	AAT	CAG	AAG	TTC	AAA	GGC	AAG	GCC	ACA	TTG	ACT	GCA	GAC	AAA		
																			2631																2667		2676		
75										80										82 82A 82B 82C 83										85									
Ser	Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	TCC	TCC	AGC	ACA	GCC	TAC	ATG	CAG	CTC	AGC	AGC	CTG	ACA	TCT	CAG	GAC	TCT	GCG	GTC		
																			2688																2724		2733		
90										94 95 CDR3										100 100A 100B 100C 100D 101 102 103																			
Tyr	Tyr	Cys	Ala	Arg	Ser	Thr	Tyr	Tyr	Gly	Gly	Asa	Trp	Tyr	Phe	Asn	Val	Trp	Gly	TAT	TAC	TGT	GCA	AGA	TCG	ACT	TAC	TAC	GGC	GGT	GAC	TGG	TAC	TTC	AAT	GTC	TGG	GGC		
																			2745																2781		2790		
105 FR4 110 113										Ala Gly Thr Thr Val Thr Val Ser Ala																													
																			2802																2820		2820		

FIG. 5

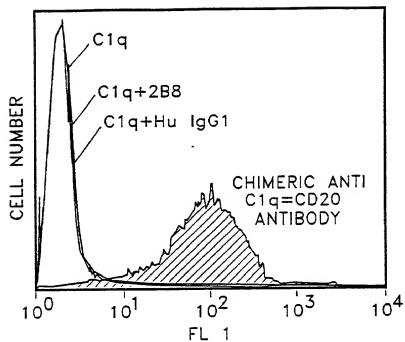


FIG. 6

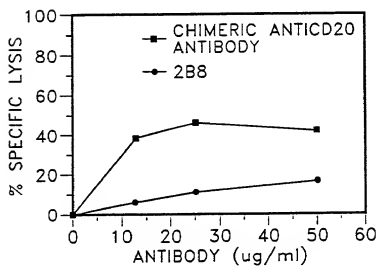


FIG. 7



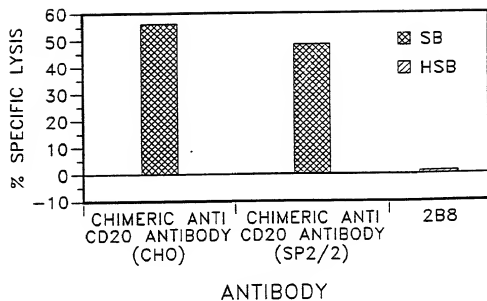


FIG. 8

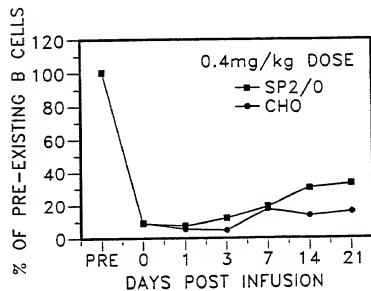


FIG. 9A

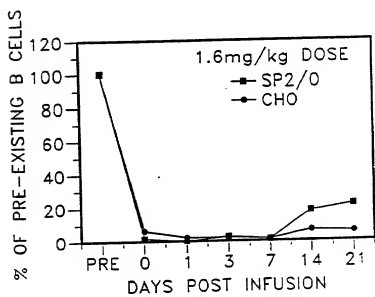


FIG. 9B

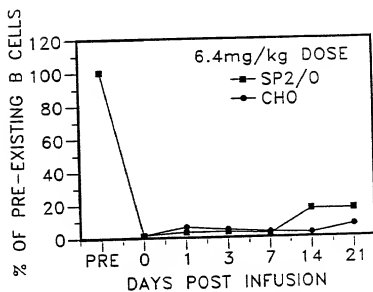


FIG. 9C

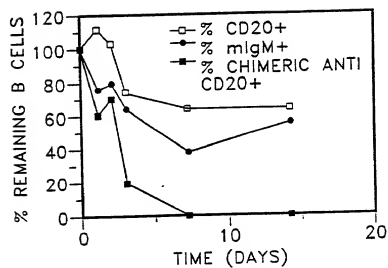


FIG. 10

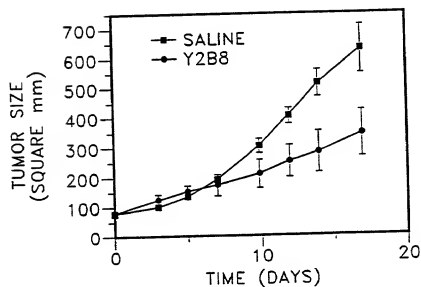


FIG. 11

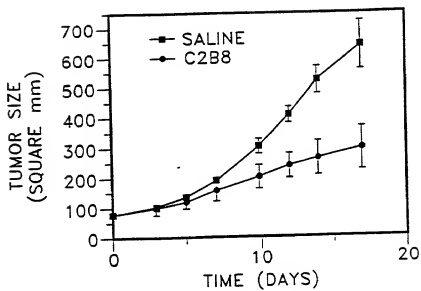


FIG. 12

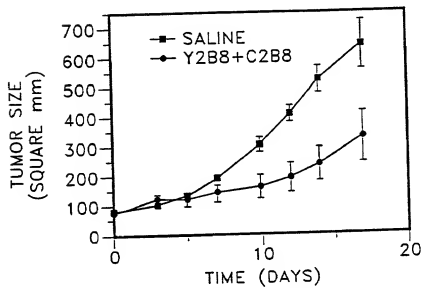


FIG. 13

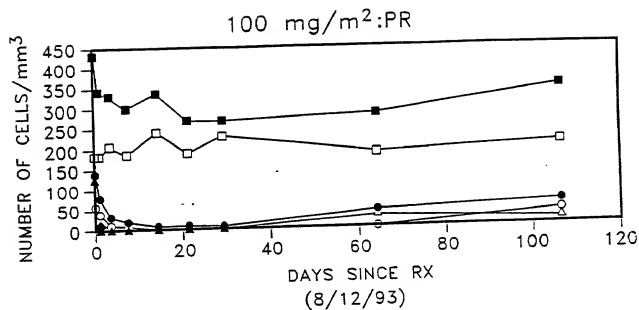


FIG. 14A

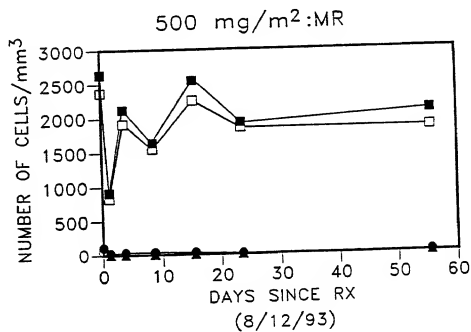


FIG. 14B